

Table S1

Subject demographics

	Age	Gender	Race/Ethnicity
Subject 1	35	Male	African American
Subject 2	31	Female	Asian
Subject 3	24	Female	Asian
Subject 4	29	Male	Caucasian

Table S2. International tooth enumeration

Tooth Number	International Enumeration
1	1.8
2	1.7
3	1.6
4	1.5
5	1.4
6	1.3
7	1.2
8	1.1
9	2.1
10	2.2
11	2.3
12	2.4
13	2.5
14	2.6
15	2.7
16	2.8
17	3.8
18	3.7
19	3.6
20	3.5
21	3.4
22	3.3
23	3.2
24	3.1
25	4.1
26	4.2
27	4.3
28	4.4
29	4.5
30	4.6
31	4.7
32	4.8

Table S3
Virome reads from each subject

	Reads							Contigs	
	Initial Count	Trimmed ^b	Low Complexity ^c	Final Count	Length ^a	16S rRNA	Human	Number	Length ^a
Subject 1									
Saliva	1,829,696	587,398	918	1,241,380	96	0	0	181	616
Plaque	721,943	99,308	0	622,635	73	0	0	676	735
Subject 2									
Saliva	1,257,920	620,965	444	636,511	85	0	0	2,094	606
Plaque	2,660,190	801,870	893	1,857,427	91	0	2	970	912
Subject 3									
Saliva	941,661	389,494	1,502	544,665	89	0	0	735	646
Plaque	2,668,766	1,503,124	1,140	1,164,502	93	0	721	1,543	695
Subject 4									
Saliva	1,295,882	536,633	102	759,147	96	0	0	838	716
Plaque	995,619	53,635	0	941,984	87	0	0	673	716

^aMean length

^bNumber of reads removed based on quality scores

^cReads removed based on multiple homopolymers

Table S4
16S rRNA reads from each subject

	Initial Count	Removed ^a	Final Count	Mean Length
Subject 1				
Saliva	23,628	9,062	14,566	172
Plaque	40,766	24,022	16,744	167
Subject 2				
Saliva	29,757	17,672	12,085	169
Plaque	38,000	19,745	18,255	165
Subject 3				
Saliva	51,090	32,895	18,195	173
Plaque	102,756	57,051	45,705	169
Subject 4				
Saliva	53,380	19,325	34,055	175
Plaque	82,079	50,964	24,779	164

^aRemoved based on length, ambiguity, quality, and homopolymers

Table S5. CRISPR repeat motifs in different streptococci

SGII	SGI
<i>S. gordonii</i>	<i>S. mutans</i>
<i>S. thermophilus</i>	<i>S. thermophilus</i>
<i>S. gallolyticus</i>	<i>S. gallolyticus</i>
<i>S. anginosus</i>	<i>S. anginosus</i>
<i>S. salivarius</i>	<i>S. salivarius</i>
<i>S. intermedius</i>	<i>S. infantarius</i>
<i>S. suis</i>	<i>S. mitis</i>
<i>S. pasteurianus</i>	<i>S. sanguinis</i>
<i>S. macedonicus</i>	<i>S. pyogenes</i>
	<i>S. agalactiae</i>
	<i>S. dysgalactiae</i>
	<i>S. equi</i>

Table S6**Streptococcal Group I (SGI) CRISPRs from each subject**

	Number of Reads	Number of Spacers	Spacer Groups	Mean Length	Median Length
Subject 1					
Saliva	43,466	25,465	207	30	30
Plaque	93,762	53,974	356	30	30
All Combined ^a	137,228	79,439	306	30	30
Subject 2					
Saliva	48,646	25,535	256	30	30
Plaque	111,734	65,717	289	30	30
All Combined ^a	160,380	91,252	349	30	30
Subject 3					
Saliva	31,479	16,844	388	30	30
Plaque	92,001	45,757	467	30	30
All Combined ^a	123,480	62,601	473	30	30
Subject 4					
Saliva	143,840	25,492	193	30	30
Plaque	121,286	34,355	301	30	30
All Combined ^a	265,126	59,847	428	30	30
All Subjects					
Saliva	267,431	93,336	957	30	30
Plaque	418,783	199,803	1,251	30	30
All Combined ^a	686,214	293,139	1,912	30	30

^aDetermined by combining all spacers prior to binning based on trinucleotide content

Table S7**Streptococcal Group II (SGII) CRISPRs from each subject**

		Number of Reads	Number of Spacers	Spacer Groups	Mean Length	Median Length
Subject 1	Saliva	81,466	24,178	105	29	30
	Plaque	121,592	36,065	378	29	30
	All Combined ^a	203,058	60,243	284	29	29
Subject 2	Saliva	25,672	16,804	316	30	30
	Plaque	153,425	32,117	469	29	29
	All Combined ^a	179,097	48,921	384	29	29
Subject 3	Saliva	27,636	16,172	254	29	30
	Plaque	128,471	53,427	509	30	30
	All Combined ^a	156,107	69,599	439	30	30
Subject 4	Saliva	40,068	15,694	199	29	30
	Plaque	220,116	34,652	180	30	30
	All Combined ^a	260,184	50,346	270	30	30
All Subjects	Saliva	174,842	72,842	750	29	30
	Plaque	623,604	156,261	1,272	29	30
	All Combined ^a	798,446	229,103	1,084	29	30

^aDetermined by combining all spacers prior to binning based on trinucleotide content

Table S8 - CRISPR spacer homologues

Sample Type Subject Number	Streptococcal Group II								Streptococcal Group I							
	Saliva 1	Plaque 1	Saliva 2	Plaque 2	Saliva 3	Plaque 3	Saliva 4	Plaque 4	Saliva 1	Plaque 1	Saliva 2	Plaque 2	Saliva 3	Plaque 3	Saliva 4	Plaque 4
Streptococcal Phage																
S. phage 040922	0	43	12	2	1	24	26	17	0	4	1	0	0	0	7	0
S. phage 11865	0	0	0	1	1	0	2	1	0	1	0	0	2	1	0	0
S. phage 2167	0	2	1	8	5	24	5	5	11	6	3	1	3	10	0	0
S. phage 34117	0	0	0	5	2	3	2	0	4	1	0	0	6	0	0	0
S. phage 5093	0	0	0	0	0	0	0	0	0	6	0	0	0	0	0	2
S. phage 7201	0	0	0	0	0	0	0	0	0	14	0	1	0	0	0	0
S. phage 8140	0	0	0	30	9	6	4	2	0	0	1	18	0	0	0	0
S. phage 858	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0
S. phage Abc2	0	0	0	0	4	0	0	1	1	0	0	0	0	0	0	0
S. phage ALQ13.2	0	0	7	0	0	0	0	0	0	2	0	2	0	0	0	3
S. phage CP1	19	3	4	11	0	57	4	14	2	31	5	6	10	41	38	29
S. phage CP7	0	0	0	0	0	7	0	0	0	0	0	0	0	0	0	0
S. phage DP1	6	26	10	15	1	5	12	2	0	22	12	9	7	4	0	0
S. phage DT1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
S. phage DT1.1	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0
S. phage EJ1	0	1	0	11	1	11	1	50	0	3	0	2	0	4	11	11
S. phage M102	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
S. phage MD2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
S. phage MM1 1998	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0
S. phage PH10	2	42	15	56	67	38	24	26	0	13	20	60	13	37	10	0
S. phage PH15	0	40	9	1	0	8	14	16	0	2	0	0	1	0	1	0
S. phage Sfi11	0	0	0	1	0	0	0	1	1	0	0	2	0	0	0	0
S. phage SM1	4	0	2	61	2	30	19	13	3	21	45	40	4	51	8	26
S. phage SMP	0	0	0	0	0	3	0	0	0	0	0	0	15	4	0	0
S. phage V22	0	0	0	2	2	20	3	0	0	5	0	0	0	1	5	25
S. phage YMC-2011	0	4	1	9	0	0	0	0	0	3	0	2	2	0	2	6

Streptococcal Plasmids and Transposons

S. plasmid 1	0	0	0	0	1	4	4	6	0	0	0	1	0	0	0	0
S. plasmid pDRPIS7493	0	0	0	0	0	0	0	0	0	0	0	0	0	2	7	22
S. plasmid pFW213	2	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0
S. plasmid pND103	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
S. plasmid pSMQ173b	0	0	0	0	0	1	1	4	0	0	0	0	0	0	0	0
S. plasmid pSMQ-316	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
S. plasmid pSpnP1	74	3	1	1	0	0	0	42	0	21	0	0	0	43	6	24
S. transposon Tn1311	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0

Streptococcal Genomes

S. gallolyticus ATCC BAA-2069	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
S. gallolyticus UCN34	0	0	0	4	0	0	0	0	0	0	0	5	0	0	0	0
S. gordonii CH1	0	0	0	0	0	5	8	15	0	0	0	0	0	0	0	0
S. mitis B6 complete genome	0	0	0	55	4	17	2	81	0	0	4	6	3	1	1	1
S. mutans UA159	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
S. oralis Uo5	0	0	0	0	0	2	0	3	0	0	0	0	0	0	0	0
S. parasanguinis ATCC 15912	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	13
S. pneumoniae 19A-6	0	1	0	1	1	0	1	1	0	0	0	1	0	0	0	0
S. pneumoniae 670-6B	0	1	0	1	0	12	8	16	0	0	0	0	1	0	0	0
S. pneumoniae 70585	0	0	0	0	0	1	0	0	0	0	0	0	2	1	1	0
S. pneumoniae AP200	0	0	0	1	0	16	14	8	0	5	1	1	1	3	6	8
S. pneumoniae ATCC 700669	7	0	0	5	0	3	0	0	0	4	3	3	1	2	1	0
S. pneumoniae G54	0	0	0	6	0	0	1	1	0	0	0	2	0	0	0	0
S. pneumoniae JJA	0	0	0	4	1	0	0	0	0	0	1	2	0	0	1	0
S. pneumoniae OXC141	0	0	0	1	0	17	3	3	12	3	2	0	10	2	0	0
S. pneumoniae P1031	0	0	0	2	0	0	1	1	0	0	1	0	0	0	0	0
S. pseudopneumoniae IS7493	0	12	1	84	4	25	4	18	20	21	4	5	11	7	11	13
S. salivarius JIM8777	0	14	1	24	1	0	0	5	0	0	0	16	2	0	30	0
S. thermophilus DGCC1443	0	0	0	2	0	0	0	0	0	3	0	1	0	0	1	0
S. thermophilus JIM 8229	0	0	0	0	0	0	0	0	0	10	0	0	0	0	0	0
S. thermophilus DGCC 7710	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0
S. thermophilus DGCC292	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
S. thermophilus DGCC66	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0

S. thermophilus DGCC766	0	0	0	5	0	1	0	0	0	5	0	3	0	0	0	10
S. thermophilus DGCC7796	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	145
S. thermophilus DGCC7809	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	11
S. thermophilus DGCC7984	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
S. thermophilus JIM 8230	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
S. thermophilus LMG 18311	0	0	0	0	0	2	2	1	0	0	0	0	0	0	0	0
S. thermophilus ND03	0	0	0	0	0	0	0	0	1	4	0	0	0	0	0	0
S. thermophilus WTphi858phi297	0	0	0	0	0	2	0	0	0	13	0	1	0	2	0	8

Non Streptococci

Bacillus cereus 03BB102	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Bacillus cereus AH820	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Bacillus plasmid WSH-002	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cellulophaga algicola DSM 14237	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Clostridium botulinum E3	0	0	0	3	0	0	0	0	0	4	3	6	0	4	1	0
Clostridium difficile BI1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Clostridium difficile M120	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Clostridium tetani E88	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
Cyanothece sp. PCC 7822	0	0	0	0	0	3	0	0	0	0	0	0	0	1	0	0
Desulfobacterium sp.	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Eubacterium limosum KIST612	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
Fusobacterium nucleatum ATCC 255	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Geobacillus sp. WCH70	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Lactobacillus delbrueckii ND02	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Lactobacillus salivarius CECT 5713	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Listeria monocytogenes Clip80459	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Listeria monocytogenes FSL R2-561	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Little cherry virus 2 USA6b	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Lysinibacillus sphaericus C3-41	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Marinobacter adhaerens HP15	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Neisseria gonorrhoeae MS11	0	2	1	0	0	6	0	0	0	0	0	0	2	6	0	0
Pediococcus pentosaceus ATCC 25745	0	0	0	0	0	2	1	2	0	0	0	0	0	0	0	0

Table S9. CRISPR Repeat Motifs and Primers

Name		
Streptococcus (SGII)^a	Consensus	GTTGTACAGTTACTTAAATCTTGAGAGTACAAAAAC
	Forward	CCATCTCATCCCTGCGTGTCTCCGACTCAGXXXXXXXXXXCAGTTACTTAAATCTTGAGAG
	Reverse	CCTCTCTATGGGCAGTCGGTGATAGATTTAAGTAAGTACTGTACAAC
Streptococcus (SGI)^b	Consensus	GTTTTGGAACCATTTCGAAACAACACAGCTCTAAAAC
	Forward	CCATCTCATCCCTGCGTGTCTCCGACTCAGXXXXXXXXXXCGTTTACGGTATTGAAAC
	Reverse	CCTCTCTATGGGCAGTCGGTGATGGTAAGCACTGTTGCAAC

^aIdentified from *Streptococcus gordonii*

^bIdentified from *Streptococcus mutans*

^cX's represent the location of the barcode sequence

Table S10**Barcode adaptors for primers**

Barcode Number	Barcode Sequence
Viromes	
1	ACGAGTGCGT
2	ACGCTCGACA
3	AGACGCACTC
4	AGCACTGTAG
5	ATCAGACACG
6	ATATCGCGAG
7	CGTGTCTCTA
8	CTCGCGTGTC
9	TAGTATCAGC
10	TCTCTATGCG
11	TGATACGTCT
16S rRNA or CRISPRs	
1	ACGAGTGCGT
2	ACGCTCGACA
3	AGACGCACTC
4	AGCACTGTAG
5	ATCAGACACG
6	ATATCGCGAG
7	CGTGTCTCTA
8	CTCGCGTGTC
9	TAGTATCAGC
10	TCTCTATGCG
11	TGATACGTCT
12	TACTGAGCTA
13	CATAGTAGTG
14	CGAGAGATAC
15	ATACGACGTA
16	TCACGTACTA
17	CGTCTAGTAC
18	TCTACGTAGC
19	TGTACTACTC
20	ACGACTACAG
21	CGTAGACTAG
22	TACGAGTATG
23	TACTCTCGTG